

Prevalence of Bacteria among Domestic Dogs in Port Harcourt Metropolis

Chuku, W*., Akani, N.P., Sampson, T., and Nrior, R.R.

Department of Microbiology, Rivers State University, P.M.B. 5080, Port Harcourt, Nigeria

*Corresponding Author: wobarerer.chuku@ust.edu.ng

ABSTRACT

Domestic dogs (*Canis lupus familiaris*) are the most common domesticated animals globally, with their proximity to human creating an avenue for transfer of zoonotic infections. This study was aimed at assessing the prevalence of bacteria associated with domestic dogs in Port Harcourt Metropolis, Rivers State, Nigeria. A well-structured questionnaire was administered to consented dog owners from six (6) locations; Port Harcourt Town, Mgbuoba, Oroazi, Diobu, Rumuomasi, and Woji. Breeds sampled include Lhasa Apso, German Shepard German-Caucasian, Pit-bull, Chow-chow, Samoyed, Rottweiler, Aspin, Caucasian, Rottweiler-Canecosor, and Mongrel-Rottweiler. With the aid of sterile swab sticks, 200 samples were randomly collected from the skin, mouth, ear and anus of 50 domestic dogs, male and female inclusive. Samples were analysed using standard microbiological techniques. Results of bacterial isolates belonging to 12 genera and frequency were; *Proteus* spp. (78%), *Klebsiella* spp. (30%), *Salmonella* spp. (46%) *Enterobacter* spp. (82%) *Edwardsiella* spp. (28%), *Escherichia* spp. (86%), *Kluyvera* spp. (90%), *Bacillus* spp. (96%) *Paenbacillus* spp. (48%) *Micrococcus* spp. (56%) *Staphylococcus* spp. (100%) and *Kocuria* spp. (12%). These bacteria are known potential pathogens. Prevalence of bacteria across the breeds was highest in Aspin (100%), Pit-bull (100%), and German shepherd (100%). Male dogs (100%) showed a higher bacterial population than females (92%). The anus (85%) had the highest distribution of bacterial isolates, followed by ear (81%), mouth (78%) and skin (78%). Diobu (21%) and Port Harcourt Town (21%) locations recorded the highest distribution of bacterial while Rumuomasi (10%) had the least. Health care routine of the dogs affected bacterial distribution as daily bath (58%) recorded the least bacterial isolates compared to monthly, and quarterly bath (100% each). Presence of potential pathogens in this study emphasizes need for caution in interacting with domestic dogs, to minimize the spread of zoonotic infections and other associated public health risk.

Keywords: Domestic dogs, pathogens, zoonotic infections, *Kocuria* spp., *Salmonella* spp, public health risk.

Introduction

Domestic dogs, scientifically known as *Canis lupus familiaris*, are one of the most widespread and diverse species of domesticated animals globally (Azuonwu *et al.*, 2023). They belong to the Canidae family, which also includes wolves, foxes, and other related species. Dogs have been domesticated for thousands of years, with evidence suggesting domestication may have occurred as early as 15,000 years ago (Azuonwu *et al.*, 2020). Dogs come in different shapes, sizes, colors, and coat types, reflecting their long history of selective breeding for various purposes, including companionship, work, hunting, and herding (Gado *et al.*, 2023). They are highly social animals, with a strong ability to form bonds with humans and other animals (Katagiri & Oliviera-Sequeira, 2008).

Dogs have keen senses, including excellent olfactory capabilities, making them valuable for tasks such as detection, search rescue, and tracking (Ogugua *et al.*, 2017). They are known for their adaptability to various environments, from urban settings to rural landscapes, and their ability to thrive in diverse climates and conditions (Rautenbach *et al.*, 1991). Dogs serve various roles in human society, including as pets, working animals, service animals, and therapy animals (Ma *et al.*, 2020). As pets, dogs provide companionship, emotional support, and security to millions of people worldwide, contributing to their physical and mental well-being (Ogugua *et al.*, 2017).

The microbiome of the dog is composed of different microorganisms including; bacteria, archaea, fungi, protozoa and viruses.

The microbiome aid in immune system modulation digestion and nutrient absorption, production of vitamins and hormones and maintenance of barrier function (Turnbaugh *et al.*, 2007 Kim *et al.*, 2025). Factors such as diet, age, breed, environment, health status, socio-economic status, and local practices may influence the composition and diversity of the canine microbiome in Nigeria (Suchodolski *et al.*, 2012; Sandri *et al.*, 2017 and Suchodolski 2022). Microorganisms associated with domestic dogs encompass a wide range of pathogens with implications for animal and public health (Lucero *et al.*, 2010). Domestic dogs can harbor various bacteria that have the potential to cause infections in both dogs and humans. These zoonotic bacteria can be transmitted from dogs to humans through direct contact, saliva, feces, or contaminated surfaces (Gado *et al.*, 2023). *Salmonella* spp can be found in the gastrointestinal tracts of dogs and are a potential source of foodborne illness in humans. Seepersadsingh *et al.* (2004) identified *Salmonella* spp. in fecal samples from domestic dogs in Nigeria, highlighting the zoonotic potential of these bacteria. A study by Okoh *et al.* (2010) isolated pathogenic strains of *E. coli* from diarrheic dogs in Nigeria, emphasizing the importance of understanding the role of dogs in the transmission of enteric pathogens. In Nigeria, rabies remains a significant public health concern, with domestic dogs serving as the primary reservoir (Okoh *et al.*, 2010). Vaccination programs targeting domestic dogs are essential for rabies control and prevention (Oboegbulem *et al.*, 2010). Hookworms (*Ancylostoma* spp.) are intestinal parasites commonly found in dogs, particularly in tropical regions like Nigeria, these parasites can cause gastrointestinal disease and anemia in dogs and can also infect humans through skin contact (Udobi *et al.*, 2016). External parasites such as ticks and fleas are prevalent in domestic dogs in Nigeria and can transmit various pathogens, including bacteria and protozoa, causing diseases such as tick-borne fever and flea-borne typhus (Ezeifeke & Nwosu, 2015).

Proper care and management are essential for maintaining the health and well-being of domestic dogs (Pereira & Clemente 2021). This includes providing balanced nutrition, regular exercise, grooming, veterinary care, and socialization. Preventive measures, such as vaccinations, parasite control, and dental care, protect dogs from diseases.

Responsible pet ownership involves meeting dogs' physical, social, and emotional needs, as well as adhering to local regulations regarding licensing, confinement, and behavior. These in turn will reduce the risk of zoonotic infections on the handlers or owners which could result in public health challenges (Lucero *et al.*, 2010). Therefore to ensure public health and safety of dog owners or handlers this study was aimed at accessing the prevalence of bacteria associated with domestic dogs in Port Harcourt metropolis.

Materials and Methods

Study area and Dog Breeds Sampled

This study area was Port Harcourt Metropolis, Rivers State, Nigeria. A well-structured questionnaire was administered to consented dog owners from six (6) locations within Port Harcourt Metropolis, namely; Port Harcourt Town, Mgbuoba, Oroazi, Diobu, Rumuomasi, and Woji. Dog breeds sampled include Lhasa Apso, German Shepard German-Caucasian, Pit-bull, Chow-chow, Samoyed, Rottweiler, Aspin, Caucasian, Rottweiler-Canecosor, and Mongrel-Rottweiler, male and female inclusive.

Study Design

The study was a cross sectional study using convenience sampling technique due to willingness and availability (Nikolopoulou, 2023).

Inclusion Criteria

The study included domestic dogs living as household pets and security dogs whose owners agreed to participate in the study. However, the exclusion criteria include those who could not give their consent to participate in the study and none household dogs or stray dogs.

Sampling Technique

With the use of the convenient sampling technique, and sterile cotton wool swabs, samples were collected from the skin, mouth, ear and anus of 50 domestic dogs giving a total of 200 swab samples. Collected samples were kept in ice packs to prevent or reduce deterioration during transportation to Lab for analysis.

Isolation of Microbial Isolates

Isolation of bacteria from the different dog samples collected was carried out in the laboratory with the use of Nutrient Agar, Manitol Salt Agar (MSA), Eosine Methylene Blue (EMB) and MacConkey Agar (MA) (Azuonwu *et al.*, 2020) on the same day that they were collected.

Characterization and Identification of Isolates

Bacterial isolates from the samples were characterized using standard procedure as described by Bergey's manual of determinative bacteriology (Ameh & Kawo, 2018; Ghosh *et al.*, 2022). The isolates were subjected to gram stain, microscopic examination, and biochemical tests such as catalase, citrate, indole, oxidase, methyl red, Voges-Proskauer and sugar fermentation test with sucrose, glucose, lactose and mannose.

Results

Demography of Dogs studied

The demographic result of the dogs showed a total of 12 breeds of dogs were sampled in the course of this study (Figure 1). The breeds were; Lhasa Apso (32%), German Sheppard (10%), German-Caucasian (8%), Pit-bull (6%), Chow-chow (2%), Samoyed (2%), Rottweiler (10%), Aspin (16%), Caucasian (4%), Rottweiler-Canecoso (4%), Rottweiler-Caucasian (4%) and Mongrel-Rottweiler (2%), Lhasa Apso was the highest bred sampled next to Aspin (local dogs).

The gender distribution of the dogs studied indicates that male dogs (76%) were more than the female (24%). From the data obtained from dog owners it was observed that the dogs studied were mostly used as companion dogs (46%) and security dogs (32%) while few were used as both companion and security dogs (22%).

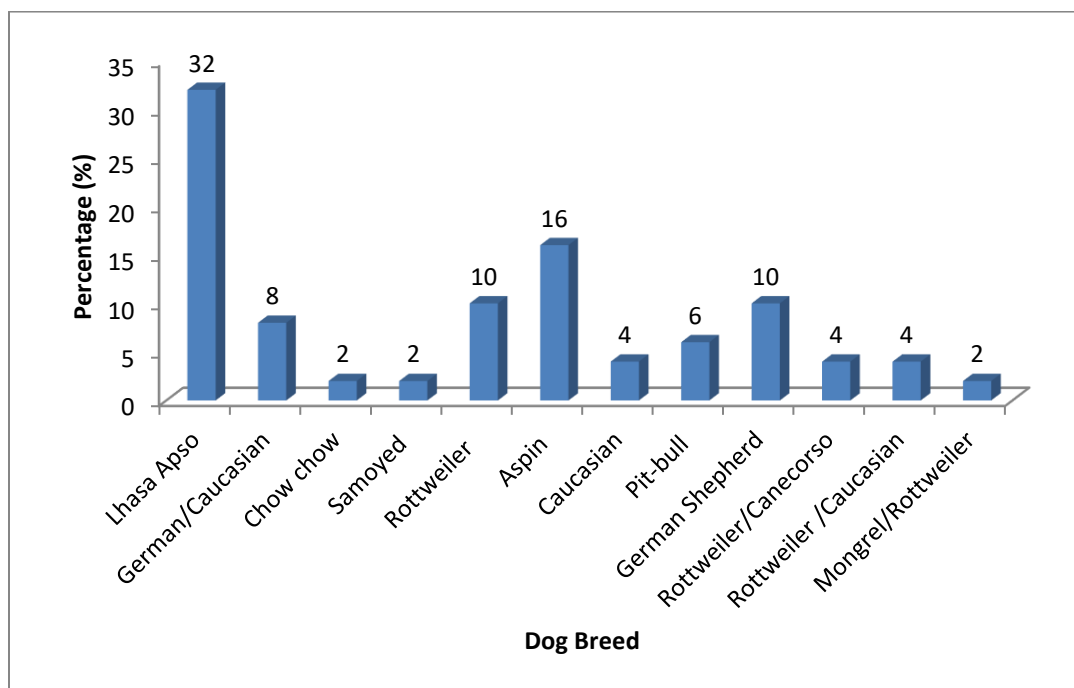


Figure 1: Breeds of the Dogs Studied

The age distribution of the dogs studied is as presented in Figure 2. The findings indicated that most of the dogs studied were within the age bracket of 2-4yrs

(52%), followed by 0-2yrs (36%) with age bracket 10-12yrs (2) having the least value.

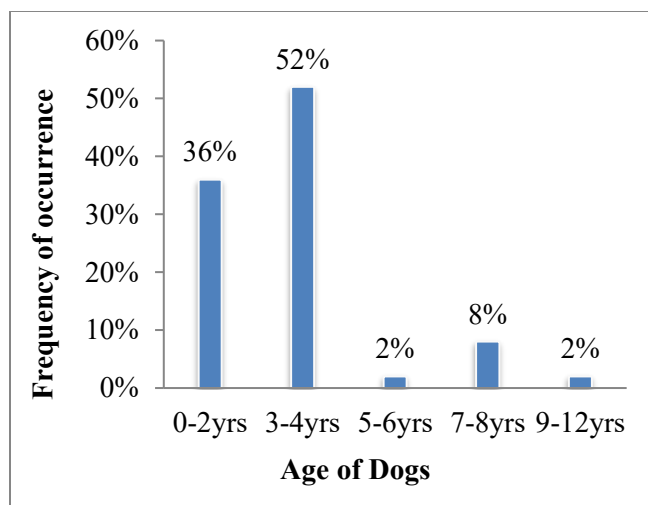


Fig. 2: Age Distribution of the Dogs Studied

Table 1: Prevalence of Bacteria Isolates in the Different Parts of the Dogs Studied

S/N	Isolated Organism	Body Part of Dog Sampled			
		Skin n=50 (%)	Mouth n=50 (%)	Ear n=50 (%)	Anus n=50 (%)
1	<i>Staphylococcus</i> spp	47(94)	34(68)	33(66)	42(84)
2	<i>Bacillus</i> spp	27(54)	08(16)	17(34)	37(74)
3	<i>Escherichia</i> spp	23(46)	10(20)	18(36)	22(44)
4	<i>Klebsiella</i> spp	04(08)	01(02)	02(04)	09(18)
5	<i>Kluyvera</i> spp	13(26)	31(62)	22(44)	17(34)
6	<i>Enterobacter</i> spp	05(10)	37(74)	12(24)	09(18)
7	<i>Proteus</i> spp	08(16)	08(16)	27(54)	18(36)
8	<i>Micrococcus</i> spp	04(08)	16(32)	11(22)	04(08)
9	<i>Edwardsiella</i> spp	04(08)	01(02)	03(06)	07(14)
10	<i>Salmonella</i> spp	02(4)	18(36)	06(12)	03(6)
11	<i>Paenbacillus</i> spp	15(30)	01(2)	10(20)	00(0)
12	<i>Kocuria</i> spp	03(6)	00(0)	00(0)	01(2)
Total n = 200(%)		155 (77.5)	155(77.5)	161(80.5)	169(84.5)

Table 2 presents the distribution of the bacteria in dogs from the locations sampled. Results indicated Port Harcourt town (21%) and Diobu (21%) as the locations with the highest distribution and Rumuomasi (10%) as the least.

In the study it was also observed that the distribution of bacterial isolates was highest in male dogs (100%) compared to female dogs (92%) and all *Kocuria* spp. isolated was isolated from only male dogs, this is shown in Figure 3.

Prevalence of Bacterial Isolates

Results showed bacterial isolates belonging to 12 genera were identified; *Proteus* spp. (78%), *Klebsiella* spp. (30%), *Salmonella* spp. (46%) *Enterobacter* spp. (82%) *Edwardsiella* spp. (28%), *Escherichia* spp. (86%), *Kluyvera* spp. (90%), *Bacillus* spp. (96%) *Paenbacillus* spp. (48%) *Micrococcus* spp. (56%) *Staphylococcus* spp. (100%) and *Kocuria* spp. (12%).

The distribution of organisms in respect to different parts of dogs sampled is shown in Table 1 and it indicates that the anus (85%) had the highest distribution of bacterial isolates followed by the ear (81%) the skin (78%) and mouth (78%).

Amongst the dogs sampled, the breeds that exhibited the highest bacterial population were the Aspin (100%), pit-bull (100%) and German shepherd (100%) as evidently displayed in Table 3.

Table 4a and 4b shows the hygiene routine of the dogs studied and their effect on the bacterial population of the dogs with the result showing that dogs with a more regular health routine had the least bacterial population.

Table 2: Prevalence of Bacterial Isolates in Dogs from the Locations Studied

Organism	Location						
	PH Town n=10 (%)	Woji n=6 (%)	Oroazi n=9 (%)	Diobu n=11 (%)	Mbuogba n=8 (%)	Rumuomasi n=6 (%)	Overall n = 50 (%)
<i>Staphylococcus</i> spp	10(100)	06(100)	09(100)	11(100)	08(100)	06 (100)	50 (100)
<i>Bacillus</i> spp	10(100)	06(100)	09(100)	11(100)	07(88)	05(83)	48(96)
<i>Escherichia</i> spp	08(80)	05(83)	06(67)	10(91)	08(100)	06(100)	43(86)
<i>Klebsiella</i> spp	03(30)	03(50)	03(33)	02(18)	04(50)	00(00)	15(30)
<i>Khuyvera</i> spp	09(90)	05(83)	08(89)	11(100)	07(88)	05(83)	45(90)
<i>Enterobacter</i> spp	10(100)	05(83)	07(78)	09(82)	08(100)	02(33)	41(82)
<i>Proteus</i> spp	09(90)	04(67)	08(89)	08(73)	07(88)	03(50)	39(78)
<i>Micrococcus</i> spp	05(50)	02(33)	06(67)	08(73)	03(38)	04(67)	28(56)
<i>Edwardsiella</i> spp	03(30)	02(33)	04(44)	02(18)	02(25)	01(17)	14(28)
<i>Salmonella</i> spp	07(70)	03(50)	01(11)	05(45)	05(63)	02(33)	23(46)
<i>Paenbacillus</i> spp	05(50)	04(67)	06(67)	02(18)	05(63)	02(33)	24(48)
<i>Kocuria</i> spp	01(10)	00(00)	01(11)	01(09)	03(38)	00(00)	6(12)
Total (%) n= 376	80(21)	45(12)	68(18)	80(21)	67(18)	36(10)	376(100)

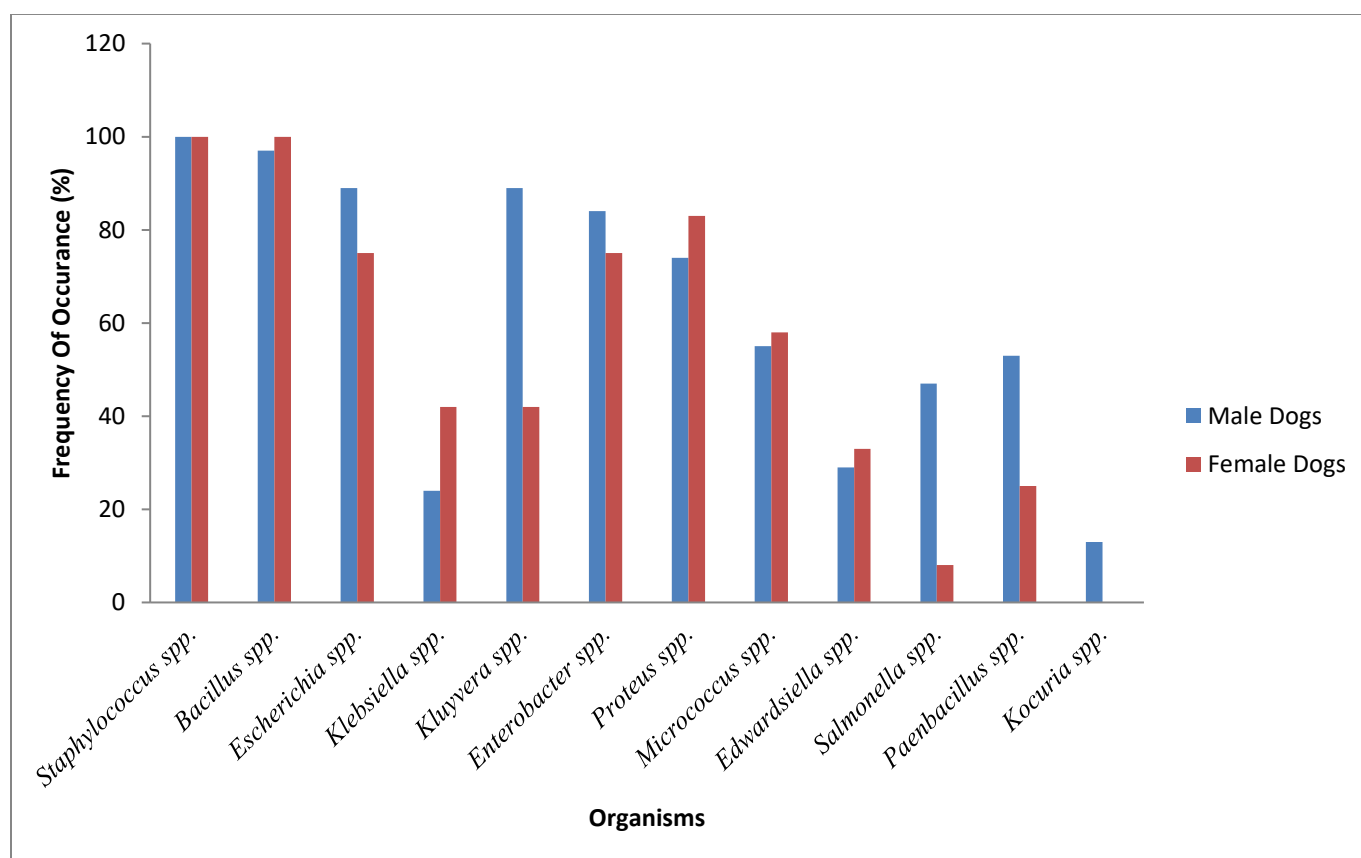


Fig. 3: Prevalence of Bacterial Isolates According to Gender of Dogs Studied

Table 3: Prevalence of Bacteria Isolates across Different Dog Breeds Studied

Organisms	Lhasa n=16(%)	Cau/Ger n=4(%)	Chow n=1(%)	Samoyed n=1(%)	Rottweiler n=5(%)	Aspin n=8(%)	Caucasian n=2(%)	Pitbull n=3(%)	Ger/Shep n=5(%)	Rot/Cane n=2(%)	Rot/Cau n=2(%)	Mon/Rot n=1(%)
<i>Staphylococcus</i> spp.	16(100)	4(100)	1(100)	1(100)	5(100)	8(100)	2(100)	3(100)	5(100)	2(100)	2(100)	1(100)
<i>Bacillus</i> spp.	16(100)	4(100)	1(100)	1(100)	5(100)	8(100)	1(50)	3(100)	5(100)	2(100)	1(50)	1(100)
<i>Escherichia</i> spp.	13(81)	4(100)	1(100)	1(100)	5(100)	8(100)	2(100)	3(100)	4(80)	1(50)	1(50)	0
<i>Klebsiella</i> spp.	6(38)	1(25)	0	1(100)	1(20)	1(13)	0	2(67)	2(40)	0	2(100)	0
<i>Kluyvera</i> spp.	15(94)	4(100)	1(100)	1(100)	5(100)	7(88)	1(50)	2(67)	3(60)	2(100)	2(100)	1(100)
<i>Enterobacter</i> spp.	14(88)	2(50)	0	1(100)	3(60)	8(100)	1(50)	2(67)	5(100)	2(100)	2(100)	1(100)
<i>Proteus</i> spp.	12(75)	3(75)	1(100)	1(100)	3(60)	7(88)	1(50)	2(67)	5(100)	1(50)	1(50)	1(100)
<i>Micrococcus</i> spp.	7(44)	2(50)	1(100)	1(100)	4(80)	4(50)	1(50)	2(67)	3(60)	1(50)	1(50)	0
<i>Edwardsiella</i> spp.	6(38)	3(75)	0	0	1(20)	1(13)	0	1(33)	1(20)	1(50)	1(50)	0
<i>Salmonella</i> spp.	8(50)	1(25)	0	0	3(60)	4(50)	1(50)	1(33)	3(60)	1(50)	1(50)	0
<i>Paenbacillus</i> spp.	4(25)	2(50)	0	0	1(20)	6(75)	1(50)	3(100)	4(80)	1(50)	0	1(100)
<i>Kocuria</i> spp.	0	0	0	0	0	1(13)	0	1(33)	1(20)	1(50)	1(50)	0
Total n=12(%)	11(92)	11(92)	6(50)	8(67)	11(92)	12(100)	9(75)	12(100)	12(100)	11(92)	11(92)	6(50)

Key: Lhasa= Lhasa Apso; Cau-Ger = Caucasian-Shepard; Chow = Chow Chow; Ger-Shep = German Shepard; Rot/Cane = Rottweiler-Canecorso; Rot-Cau = Rottweiler/ Caucasian; Mon/Rot = Mongrel-Rottweiler.

Table 4a: Distribution of Bacterial Isolates According to Health Care Routine of the Dogs Studied

Organism	Daily			Weekly			Monthly			Quarterly		
	Bath n=1	TR n=3	Vet n=0	Bath n=23	TR n=12	Vet n=0	Bath n=16	TR n=7	Vet n=22	Bath n=7	TR n=9	Vet n=19
<i>Staphylococcus</i> spp.	1	3	0	23	12	0	16	7	22	7	9	19
<i>Bacillus</i> spp.	1	3	0	23	12	0	15	7	22	6	9	19
<i>Escherichia</i> spp.	1	2	0	19	9	0	11	3	10	7	7	16
<i>Klebsiella</i> spp.	0	1	0	5	2	0	5	3	8	1	6	4
<i>Kluyvera</i> spp.	1	3	0	21	11	0	15	6	21	4	9	17
<i>Enterobacter</i> spp.	1	2	0	17	7	0	15	6	20	5	9	15
<i>Proteus</i> spp.	0	2	0	17	8	0	13	6	18	5	8	14
<i>Micrococcus</i> spp.	1	3	0	15	10	0	6	2	10	3	4	14
<i>Edwardsiella</i> spp.	0	0	0	6	4	0	6	2	7	3	3	4
<i>Salmonella</i> spp.	1	1	0	8	3	0	8	3	8	3	4	9
<i>Paenbacillus</i> spp.	0	0	0	8	3	0	8	4	10	6	5	9
<i>Kocuria</i> spp.	0	0	0	2	1	0	1	1	4	2	1	0
Total n=12(%)	7(58)	9(75)	0	12(100)	12(100)	0	12(100)	12(100)	12(100)	12(100)	12(100)	11(92)

Key: TR = Use of Tick Remover; Vet = Veterinary Care

Table 4b: Distribution of Bacterial Isolates According to Health Care Routine of the Dogs Studied

Organisms	Health Care Routine of the Dogs								
	Biannually			Annually			Never		
	Bath n=3	TR n=3	Vet n=4	Bath n=0	TR n=0	Vet n=2	Bath n=0	TR n=16	Vet n=3
<i>Staphylococcus</i> spp.	3	3	4	0	0	2	0	16	3
<i>Bacillus</i> spp.	3	3	4	0	0	2	0	15	2
<i>Escherichia</i> spp.	2	2	3	0	0	2	0	15	2
<i>Klebsiella</i> spp.	2	2	2	0	0	0	0	1	1
<i>Kluyvera</i> spp.	3	3	3	0	0	1	0	13	3
<i>Enterobacter</i> spp.	3	3	4	0	0	0	0	14	2
<i>Proteus</i> spp.	3	3	4	0	0	1	0	10	1
<i>Micrococcus</i> spp.	1	1	1	0	0	0	0	7	2
<i>Edwardsiella</i> spp.	0	0	0	0	0	1	0	4	2
<i>Salmonella</i> spp.	2	2	2	0	0	0	0	8	1
<i>Paenbacillus</i> spp.	1	1	2	0	0	2	0	10	1
<i>Kocuria</i> spp.	0	0	1	0	0	0	0	2	1
Total n=12(%)	10(83)	10(83)	11(92)	0	0	7(58)	0	12(100)	12(100)

Key: TR- Use of Tick Remover; Vet-Veterinary Care

Discussion

This study has revealed the socio-demographics and prevalence of bacteria in different body parts of domestic dogs in six locations of Port Harcourt Metropolis. In this study microorganisms similar to those described in previous studies were identified, in addition some isolates not commonly associated with dogs were also identified, they include *Edwardsiella* spp., a gram negative bacteria that acts as pathogens in aquatic environment but can cause opportunistic infections in human (Reichley *et al.*, 2017). *Paenbacillus* spp., reported to be environmental isolates that have potentials to be pathogenic to human, they are also observed to exhibit high multiple antibiotics resistance (Sáez-Nieto *et al.*, 2017). *Kocuria* spp are gram positive bacteria often found as normal flora in human but have lately been associated with infections in human (Ziogou *et al.*, 2023) and *Kluyvera* spp. a gram negative bacteria commonly found in the environment and are observed to act as opportunistic pathogens in human (Apurva *et al.*, 2024). The presence of these organisms on the dogs sampled could be as a result of transfer from environment or from the human handlers to the dogs.

The results showed that *Staphylococcus* spp. was evident in every dog sampled and from every location, this was closely followed by *Bacillus* spp.

This concurs with previous work in which *Staphylococcus* and *Bacillus* species were identified as some of the isolates from domestic dog (Thomson *et al.*, 2022). Out of the 6 locations sampled, PH Town and Diobu had the highest distribution of organisms. This could be as a result of how densely populated and the fact that the dogs sampled from this location were mostly allowed to roam freely (Smith *et al.*, 2019). Among the dogs studied, those fed with strict dog food diet had a greater distribution of microorganisms isolated compared to those with varying diet, it also agrees with the study carried out by Bernaquez *et al.*, (2025) that observed that dogs with diets comprising of raw meat are carriers of high microbial load, and some of the dog feed referred to in this current study are made up of slightly cooked meet chunks that could still be contaminated with organisms associated with raw meat. Although studies have shown that when domestic dogs, share same food, living areas and lifestyle with their owners their microbiota tend to mimic that of their owners (Hernandez *et al.*, 2022). This could be responsible for the microbial load of dogs fed with same food as the owners.

The result of this study also showed that the dogs' health care routine played a role in the microbial distribution among the dogs studied as it was observed that dogs with daily health care routine had the least distribution of organisms.

This supports previous study that highlights the need for regular hygiene by dog owner and handlers after interaction with their pets (Alho *et al.*, 2018). The distribution of bacteria was highest in the breed Aspin (local dogs) pit-bull, and German shepherd, this could be because most of these breeds were used more for security purposes than pets and possible were not given as much care as the pets dogs that had more access to the living quarters and personal items of the owners and handlers and previous studies have shown that security dogs or guard dogs have been observed to have a higher microbial load than the companion dogs (Adeiza *et al.*, 2023; Azuonwu *et al.*, 2023 Gruenberger *et al.*, 2023). The bacterial distribution according to gender of the dogs revealed that the distribution of bacterial isolates was slightly higher in the male than in the female dogs. This is attributed to the fact that female dogs are more protected than the males as owners tend to protect the females in order to regulate reproduction.

The anus and ear had the greatest concentration of microorganisms identified. This could be due to the less attention being given to these areas or body parts in regards to dog care and hygiene. Since no one will intentionally have contact with the anus of the dog without conscious effort to wash afterwards. The ear on the other hand is a cause for concern as it is a part of the pet dog that owners and handlers touch regularly. *Kocuria* spp. is the only isolate that was not isolated from female dogs, but they are said to be the normal skin and mucus membrane microbiota of animals and human (Kandi *et al.*, 2016).

The different health care routine of the different dogs sampled had a role to play in the distribution of organism, as the dog with daily care had the least distribution of organism compared with dogs with yearly health care or none existing health care routine. This concurs with the study carried out by Dorji *et al.*, (2020) who observed that stray dogs are more exposed to be carriers of organisms of public health risk due to the lack of care of any kind be it regular hygiene like regular baths or veterinary care in which they have their monthly or quarterly vaccines to help their overall health. Although a study by Discepolo *et al* (2023) concluded that daily bathing could disrupt the canine dermal microbiota with negative impact to dermal health as it could lead to loss of beneficial organisms creating room for opportunistic pathogens.

Conclusion

The findings of this study revealed the presence of 12 bacteria genera associated with pathogenicity in humans as well as animals. The bacteria included *Proteus* spp., *Klebsiella* spp., *Salmonella* spp., *Enterobacter* spp., *Edwardsiella* spp., *Escherichia* spp., *Kluyvera* spp., *Bacillus* spp., *Paenbacillus* spp., *Micrococcus* spp., *Staphylococcus* spp. and *Kocuria* spp across the fifty domestic dogs sampled. The high prevalence of these bacteria in the anus, skin, mouth, and ears which are the parts of the dogs that owners and handlers make contact with regularly implies that domestic dogs could be responsible for the transfer of pathogenic organisms to their handlers and owners and *Vice versa*. Therefore it is essential that strict adherence to proper hygiene practices for the dogs and also the owners and handlers after contact with these dogs and routine veterinary care for the dogs will surely result in the reduction of microbial load on the dogs and safe guard public health

References

- Adeiza, A. M., Sani, N. A., Alhaji, N. B., Godwin, E. A., Okwolo, C. E., & Uchendu, G. (2023). Prevalence and Diversity of Zoonotic Protozoa in Dogs in Lokoja, North Central, Nigeria. *Sahel Journal of Veterinary Sciences*, 20(4), 34-40.
- Alho, A. M., Lima, C., Colella, V., Madeira de Carvalho, L., Otranto, D., & Cardoso, L. (2018). Awareness of zoonotic diseases and parasite control practices: a survey of dog and cat owners in Qatar. *Parasites & vectors*, 11(1), 133.
- Ameh, A., & Kawo, A.H. (2018). Enumeration, isolation and identification of bacteria and fungi from soil contaminated with petroleum products using layer chicken droppings as an amendment. *Bayero Journal of Pure and Applied Sciences*, 10, 219-225.
- Apurva, R., Nikhil, R., Vikramjeet, S., Das, A., & Agarwal, J. (2024). *Kluyvera ascorbata* An Emerging Pathogen and Rare Cause of Urinary Tract Infection in Immunocompetent Patients at a Tertiary Care Center in North India. *Archives of Medicine and Health Sciences*, 12(2), 255-258.

Azuonwu, O., Amadi, F. O, Nwokah, G E., Onwuli, D, Reuben, E., Orabueze, I.C., Azuonwu, G., Poplong, A.N., Tamuno-Boma, O. John-Amadi, V.S., Ekwuozor, I.K. & Agala, V. (2023). Distribution of Some Potential Pathogenic Microbial Risk Pathogens amongst Pet Dogs in Port Harcourt Metropolis: A Critical Public Health Community Alert, *International Journal of Clinical Epidemiology*, 2(2); DOI:10.31579/2835-9232/013

Azuonwu, O., Kemsu, B., Njoku-Tony, R.F. & Wokem, G.N. (2020). Investigation of Emerging Risk Factors and Isolation of Potential Pathogenic Bacteria from Domestic Dog Stool in Port Harcourt Metropolis, Niger Delta. *Journal of Zoological Research*, 1(2), 1-13.

Bernaquez, I., Dumaresq, J., Picard, I., Gaulin, C., Dion, R., Weaver, K., Walker, M., Kearney, A., Bharat, A., Fafard J., & Bekal, S. (2025). Dogs fed raw meat-based diets are vectors of drug-resistant *Salmonella* infection in humans. *Communications Medicine*, 5, 214.

Discepolo, D., Kelley, R., Watson, A., & Perry, E. (2023). Impacts to canine dermal microbiota associated with repeated bathing. *Frontiers in veterinary science*, 10, 1204159.

Dorji, T., Tenzin, T., Tenzin, K., Tshering, D., Rinzin, K., Phimpraphai, W., & de Garine-Wichatitsky, M. (2020). Seroprevalence and risk factors of canine distemper virus in the pet and stray dogs in Haa, western Bhutan. *BMC veterinary research*, 16(1), 135.

Ezeifeka, G. O., & Nwosu, C. O. (2015). Prevalence of ectoparasites infestation in dogs in Umuahia, Abia State, Nigeria. *Journal of Veterinary Medicine and Animal Health*, 7(10), 361-364.

Gado, D. A., Ehizibolo, D. O., Meseko, C. A., Anderson, N. E., & Lurz, P. W. W. (2023). Review of Emerging and Re-Emerging Zoonotic Pathogens of Dogs in Nigeria: Missing Link in One Health Approach. *Zoonotic Diseases*, 3(2), 134-161.

Ghosh, T. S., Shanahan, F., & O'Toole, P. W. (2022). The gut microbiome as a modulator of healthy ageing. *Nature reviews. Gastroenterology & hepatology*, 19(9), 565–584.

Gruenberger, I., Liebich, A.-V., Ajibade, T. O., Obebe, O. O., Ogbonna, N. F., Wortha, L. N., Unterköfler, M. S., Fuehrer, H-P., & Ayinmode A. B. (2023) Vector-Borne Pathogens in Guard Dogs in Ibadan, Nigeria. *Pathogens*, 12(3), 406.

Hernandez, J., Rhimi, S., Kriaa, A., Mariaule, V., Boudaya, H., Drut, A., Jablaoui, A., Mkaouar, H., Saidi, A., Biourge, V., Borgi, M. A., Rhimi, M., & Maguin, E. (2022). Domestic Environment and Gut Microbiota: Lessons from Pet Dogs. *Microorganisms*, 10(5), 949.

Kandi, V., Palange, P., Vaish, R., Bhatti, A. B., Kale, V., Kandi, M. R., & Bhoomagiri, M. R. (2016). Emerging Bacterial Infection: Identification and Clinical Significance of *Kocuria* Species. *Cureus*, 8(8), e731.

Katagiri, S. & Oliveira-Sequeira, T. (2008) Prevalence of dog intestinal parasites and risk perception of zoonotic infection by dog owners in São Paulo State, Brazil. *Zoonoses and Public Health*, 55(8-10), 406-13

Kim, H., Chae, Y., Cho, J. H., Song, M., Kwak, J., Doo, H., Choi, Y., Kang, J., Yang, H., Lee, S., Keum, G. B., Wattanaphansak, S., Kim, S., & Kim, H. B. (2025). Understanding the diversity and roles of the canine gut microbiome. *Journal of animal science and biotechnology*, 16(1), 95. <https://doi.org/10.1186/s40104-025-01235-4>

Lucero, N., Corazza, R., Almuzara, M., Reynes, E., Escobar, G., & Boeri, E. (2010). Human *Brucella canis* outbreak linked to infection in dogs. *Epidemiology and Infection*, 138(2), 280.

Ma, G. C., Withers, A. M., Spencer, J., Norris, J. M., & Ward, M. P. (2020). Evaluation of a Dog Population Management Intervention: Measuring Indicators of Impact. *Animals : an open access journal from MDPI*, 10(6), 1061. <https://doi.org/10.3390/ani10061061>

Nikolopoulou, K. (2023). What Is Convenience Sampling? | Definition & Examples. *Scribbr*. Retrieved April 27, 2026, from <https://www.scribbr.com/methodology/convenience-sampling/>

- Oboegbulem, S. I., Nwosuh, C. I., Okonko, I. O., & Adedeji, A. O. (2010). Prevalence of Rabies Antigen in Brain Tissue of Dogs Slaughtered for Human Consumption and Evaluation of Vaccination Program Against Rabies in Dogs in Ibadan, Oyo State, Nigeria. *Research Journal of Medicine and Medical Sciences*, 5(2), 146-151.
- Ogugua, A. J., Ogbaje, C. I., & Iroegbu, C. U. (2017). The Canine in Nigerian Environment: Management and Public Health Implications. *Nigerian Veterinary Journal*, 38(3), 229-239.
- Okoh, A. I., Sibanda, T., & Nongogo, V. (2010). Enteropathogenic *Escherichia coli* (EPEC) Associated with Diarrhea in Domestic Animals and Humans in South Africa and Nigeria. *African Journal of Biotechnology*, 9(37), 6104-6110.
- Pereira, A. M. & Clemente, A., (2021), Dogs' Microbiome From Tip to Toe, *Topics in Companion Animal Medicine*, 45, 100584,
- Rautenbach, G. H., Boomker, J., & De Villiers, I. L. (1991). A descriptive study of the canine population in a rural town in southern Africa. *Journal of the South African Veterinary Association*, 62(4), 158-162.
- Reichley, S. R., Ware, C., Steadman, J., Gaunt, P. S., García, J. C., LaFrentz, B. R., Thachil, A., Waldbieser, G. C., Stine, C. B., Buján, N., Arias, C. R., Loch, T., Welch, T. J., Cipriano, R. C., Greenway, T. E., Khoo, L. H., Wise, D. J., Lawrence, M. L., & Griffin, M. J. (2017). Comparative Phenotypic and Genotypic Analysis of *Edwardsiella* Isolates from Different Hosts and Geographic Origins, with Emphasis on Isolates Formerly Classified as *Edwardsiella tarda*, and Evaluation of Diagnostic Methods. *Journal of clinical microbiology*, 55(12), 3466–3491.
- Sáez-Nieto, J. A., Medina-Pascual, M. J., Carrasco, G., Garrido, N., Fernandez-Torres, M. A., Villalón, P., & Valdezate, S. (2017). *Paenibacillus* spp. isolated from human and environmental samples in Spain: detection of 11 new species. *New microbes and new infections*, 19, 19–27.
- Sandri, M., Dal Monego, S., Conte, G., Sgorlon, S., & Stefanon, B. (2017). Raw Meat Based Diet Influences Faecal Microbiome and End Products of Fermentation in Healthy Dogs. *BMC veterinary research*, 13(1), 65.
- Seepersadsingh, N., Adesiyun, A. A., & Seebaransingh, R. (2004). Prevalence and antimicrobial resistance of *Salmonella* spp. in non-diarrhoeic dogs in Trinidad. *Journal of veterinary medicine. B, Infectious diseases and veterinary public health*, 51(7), 337–342.
- Smith, L. M., Hartmann, S., Munteanu, A. M., Dalla Villa, P., Quinnell, R. J., & Collins, L. M. (2019). The Effectiveness of Dog Population Management: A Systematic Review. *Animals : an open access journal from MDPI*, 9(12), 1020.
- Suchodolski, J. S. (2022). Analysis of gut microbiome in dogs and cats. *Veterinary clinical pathology*, 50 (1), 6–17.
- Suchodolski, J. S., Markel, M. E., Garcia-Mazcorro, J. F., Unterer, S., Heilmann, R. M., Dowd, S. E., Kachroo, P., Ivanov, I., Minamoto, Y., Dillman, E. M., Steiner, J. M., Cook, A. K., & Toresson, L. (2012). The fecal microbiome in dogs with acute diarrhea and idiopathic inflammatory bowel disease. *PLoS one*, 7(12), e51907.
- Thomson, P., García, P., Miles, J., Isla, D., Yáñez, C., Santibáñez, R., Núñez, A., Flores-Yáñez, C., Del Río, C., & Cuadra, F. (2022). Isolation and Identification of *Staphylococcus* Species Obtained from Healthy Companion Animals and Humans. *Veterinary sciences*, 9(2), 79.
- Turnbaugh, P. J., Ley, R. E., Hamady, M., Fraser-Liggett, C. M., Knight, R., & Gordon, J. I. (2007). The human microbiome project. *Nature*, 449(7164), 804–810.
- Udobi, I. C., Anosa, V. O., & Ezeokonkwo, R. C. (2016). Prevalence of intestinal helminths of dogs in Nsukka area of Enugu State, Nigeria. *Nigerian Veterinary Journal*, 37(4), 285-290.
- Ziogou, A., Giannakodimos, I., Giannakodimos, A., Baliou, S., & Ioannou, P. (2023). *Kocuria* Species Infections in Humans-A Narrative Review. *Microorganisms*, 11(9), 2362.